

### Amendments to the Claims

Please amend existing claims and add new claims 23-26 as shown below in the List of Claims.

### List of Claims

1-12 Canceled.

13. (Currently amended) A process for the production of an L-amino acid chosen from the group consisting of L-threonine, L-isoleucine, L-valine, L-methionine, L-homoserine and L-lysine comprising:
- a) fermenting a bacterium comprising an overexpressed endogenous DNA sequence encoding the galactose-proton symporter protein in said bacterium, in a fermentation medium under conditions suitable for the production of said L-amino acid, wherein:
    - i) said bacterium is of the Enterobacteriaceae family;
    - ii) said galactose-proton symporter protein comprises the amino acid sequence of SEQ ID NO:4[[;]] and is encoded by the nucleotide sequence of SEQ ID NO:3;
    - iii) said L-amino acid is produced from glucose, saccharose, lactose, fructose, molasses, starch, cellulose or from glycerine and ethanol;
    - iv) said overexpression is achieved by increasing the copy number of said DNA or by operably linking said DNA to a promoter; and
  - b) allowing said L-amino acid to become enriched in said bacteria or said fermentation medium.
14. (Previously presented) The process of claim 13, wherein said galactose-proton symporter protein consists of the amino acid sequence of SEQ ID NO:4.
15. (Currently amended) The process of claim ~~13~~ 14, wherein said DNA sequence encoding the galactose-proton symporter protein comprises the nucleotide sequence of SEQ ID NO:3.

16. (Previously presented) The process of claim 13, wherein said DNA sequence encoding the galactose-proton symporter protein consists of the nucleotide sequence of SEQ ID NO:3.
17. (Currently amended) The process of claim 13, wherein overexpression is achieved by increasing the copy number of said DNA ~~or by operably linking said DNA to a promoter.~~
18. (Currently amended) The process of ~~any one of claims~~ claim 13[[-16]], wherein said L-amino acid is L-threonine.
19. (Previously presented) The process of any one of claims 13-16, further comprising isolating said L-amino acid along with some or all of the constituents of said fermentation medium and/or the biomass in said fermentation medium.
20. (Previously presented) The process of claim 19, wherein said L-amino acid is L-threonine.
21. (Previously presented) The process of claim 13, wherein said microorganism overexpresses one or more genes selected from the group consisting of:
  - a) the thrABC operon coding for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase;
  - b) the pyc gene coding for pyruvate carboxylase;
  - c) the pps gene coding for phosphoenolpyruvate synthase;
  - d) the ppc gene coding for phosphoenolpyruvate carboxylase;
  - e) the pntA and pntB genes coding for transhydrogenase,
  - f) the rhtB gene which imparts homoserine resistance;
  - g) the mqo gene coding for malate:quinone oxidoreductase;
  - h) the rhtC gene which imparts threonine resistance;
  - i) the thrE gene coding for threonine export protein;
  - j) the gdhA gene coding for glutamate dehydrogenase;
  - k) the glk gene coding for glucokinase;
  - l) the hns gene coding for DNA binding protein HLP-II;

- m) the pgm gene coding for phosphoglucomutase;
- n) the fba gene coding for fructose biphosphate aldolase;
- o) the ptsH gene coding for phosphohistidine protein hexose phosphotransferase;
- p) the ptsI gene coding for enzyme I in the phosphotransferase system;
- q) the crr gene coding for the glucose-specific IIA component;
- r) the ptsG gene coding for the glucose-specific IIBC component;
- s) the lrp gene coding for a regulator in the leucine regulon;
- t) the csrA gene coding for the global regulator Csr;
- u) the fadR gene coding for a regulator in the fad regulon;
- v) the iclR gene coding for a regulator in central intermediary metabolism;
- w) the mopB gene coding for the 10 KDa chaperone;
- x) the ahpC gene coding for the small sub-unit of alkyl hydroperoxide reductase;
- y) the ahpF gene coding for the large sub-unit of alkyl hydroperoxide reductase;
- z) the cysK gene coding for cysteine synthase A;
- aa) the cysB gene coding for the regulator in the cys regulon;
- bb) the cysJ gene coding for the flavoprotein in NADPH sulfite reductase;
- cc) the cysI gene coding for haemoprotein in NADPH sulfite reductase;
- dd) the cysH gene coding for adenylylsulfate reductase;
- ee) the phoB gene coding for the positive regulator PhoB in the pho regulon;
- ff) the phoR gene coding for the sensor protein in the pho regulon;
- gg) the phoE gene coding for protein E in the outer cell membrane;
- hh) the pykF gene coding for the pyruvate kinase I stimulated by fructose;
- ii) the pfkB gene coding for 6-phosphofructokinase II;
- jj) the malE gene coding for periplasmatic binding protein in maltose transport;
- kk) the sodA gene coding for superoxidedismutase;
- ll) the rseA gene coding for a membrane protein with anti-sigmaE activity;
- mm) the rseC gene coding for a global regulator in the sigmaE factor;
- nn) the sucA gene coding for the decarboxylase sub-unit of 2-ketoglutarate dehydrogenase;
- 00) the sucB gene coding for the dihydrolipoyl-transsuccinase E2 subunit of 2-ketoglutarate dehydrogenase;
- pp) the sucC gene coding for the  $\beta$ -subunit of succinyl-CoA synthetase;
- qq) the sucD gene coding for the  $\alpha$ -subunit in succinyl-CoA synthetase;

- rr) the adk gene coding for adenylate kinase;
  - ss) the hdeA gene coding for a periplasmatic protein with a chaperonin-like function;
  - tt) the hdeB gene coding for a periplasmatic protein with a chaperonin-like function;
  - uu) the icd gene coding for isocitrate dehydrogenase;
  - vv) the mglB gene coding for periplasmatic, galactose-binding transport protein;
  - ww) the lpd gene coding for dihydrolipoamide dehydrogenase;
  - xx) the aceE gene coding for the E1 component of pyruvate dehydrogenase complex;
  - yy) the aceF gene coding for the E2 component of pyruvate dehydrogenase complex;
  - zz) the pepB gene coding for aminopeptidase B;
  - aaa) the aldH gene coding for aldehyde dehydrogenase;
  - bbb) the bfr gene coding for the iron storage homoprotein;
  - ccc) the udp gene coding for uridine phosphorylase; and
  - ddd) the rseB gene coding for the regulator of sigmaE factor activity.
22. (Currently amended) The process of claim 13, wherein at least one gene in said microorganism is attenuated ~~by having its expression reduced~~, said gene being selected from the group consisting of:
- a) the tdh gene coding for threonine dehydrogenase;
  - b) the mdh gene coding for malate dehydrogenase;
  - c) the gene product of the open reading frame (ORF) yjfA;
  - d) the gene product of the open reading frame (ORF) ytfP;
  - e) the pckA gene coding for the enzyme phosphoenol-pyruvate carboxykinase;
  - f) the poxB gene coding for pyruvate oxidase;
  - g) the aceA gene coding for isocitrate lyase;
  - h) the dgsA gene coding for the DgsA regulator in the phosphotransferase system;
  - i) the fruR gene coding for fructose repressor;
  - j) the rpoS gene coding for the sigma<sup>38</sup>-Factor;

- k) the aspA gene coding for aspartate ammonium lyase; and
  - l) the aceB gene coding for malate synthase A gene.
23. (New) A process for the production of an L-amino acid chosen from the group consisting of L-threonine, L-isoleucine, L-valine, L-methionine, L-homoserine and L-lysine comprising:
- a) fermenting a bacterium comprising an overexpressed endogenous DNA sequence encoding the galactose-proton symporter protein in said bacterium, in a fermentation medium under conditions suitable for the production of said L-amino acid, wherein:
    - i) said bacterium is of the Enterobacteriaceae and transports glucose by a PEP-dependent phosphotransferase (PTS) pathway;
    - ii) said galactose-proton symporter protein comprises the amino acid sequence of SEQ ID NO:4;
    - iii) said L-amino acid is produced from glucose, saccharose, lactose, fructose, molasses, starch, cellulose or from glycerine and ethanol;
    - iv) said overexpression is achieved by increasing the copy number of said DNA or by operably linking said DNA to a promoter; and
  - b) allowing said L-amino acid to become enriched in said bacteria or said fermentation medium.
24. (New) The process of claim 23, further comprising isolating said L-amino acid along with some or all of the constituents of said fermentation medium and/or the biomass in said fermentation medium.
25. (New) The process of claim 24, wherein said bacterium is selected from the group consisting of: Escherichia coli H4581; Escherichia coli KY10935; Escherichia coli VNIIGenetika MG442; Escherichia coli VNIIGenetika M1; Escherichia coli VNIIGenetika 472T23 (US-A-5,631,157); Escherichia coli BKIIM B-3996; Escherichia coli kat 13; and Escherichia coli KCCM-10132.
26. (New) The process of claim 25, wherein said L-amino acid is L-threonine.